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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=5; day=30; hr=12; min=17; sec=48; ms=565; ]

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\*\*\*\*\*

Reviewer Comments:

<210> 30

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 30

gcttatggcg cgcctcagga ctggagcttg ctccgc

36n

21

Please delete the extra n which appears beside the total number of bases 36 and also remove the end of file text which is below the bases(21) as shown in the attachment above.

\*\*\*\*\*

Application No: 10590956 Version No: 1.0

**Input Set:****Output Set:**

**Started:** 2008-05-09 16:08:23.466  
**Finished:** 2008-05-09 16:08:25.990  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 524 ms  
**Total Warnings:** 24  
**Total Errors:** 7  
**No. of SeqIDs Defined:** 30  
**Actual SeqID Count:** 30

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)

**Input Set:**

**Output Set:**

**Started:** 2008-05-09 16:08:23.466  
**Finished:** 2008-05-09 16:08:25.990  
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**Total Warnings:** 24  
**Total Errors:** 7  
**No. of SeqIDs Defined:** 30  
**Actual SeqID Count:** 30

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
E 342	'n' position not defined found at POS: 39 SEQID(30)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 39 SEQID(30)
E 323	Invalid/missing amino acid numbering SEQID (30)at Protein (1)
E 323	Invalid/missing amino acid numbering SEQID (30) POS (1)
E 323	Invalid/missing amino acid numbering SEQID (30)at Protein (5)
E 323	Invalid/missing amino acid numbering SEQID (30)at Protein (10)
E 253	The number of bases differs from <211> Input: 36 Calculated:39

## SEQUENCE LISTING

<110> Genencor International, Inc.  
Bower, Benjamin  
Mitchinson, Colin  
Larenas, Edmund

<120> Cellulase Fusion Protein and Heterologous Cellulase Fusion  
Construct Encoding the Same

<130> GC832-PCT

<140> 10590956

<141> 2008-05-09

<150> PCT/US2005/010242

<151> 2005-03-25

<150> US 60/556,711

<151> 2004-03-25

<160> 30

<170> PatentIn version 3.2

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<211> 1570

<212> DNA

<213> Trichoderma reesei

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acttgactc aacagacagg ctccgtggtc atcgacgcca actggcgtg gactcacgct	180
acgaacagca gcacgaactg ctacgatggc aacacttggg gctcgaccct atgtcctgac	240
aacgagacct gcgcgaagaa ctgctgtctg gacggtgccg cctacgcgtc cacgtacgga	300
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acctactagt

1570

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<211> 51

<212> DNA

<213> *Trichoderma reesei*

<400> 2

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<210> 3

<211> 1438

<212> DNA

<213> *Trichoderma reesei*

<400> 3

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actcacgcta	cgaacagcag	cacgaactgc	tacgatggca	acacttgag	ctcgacccta	180
tgtcctgaca	acgagacctg	cgcgaagaac	tgctgtctgg	acggtgccgc	ctacgcgtcc	240
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cagaagaacg	ttggcgctcg	cctttacctt	atggcgagcg	acacgacctc	ccaggaattc	360
acctgcttg	gcaacgagtt	ctctttcgat	gttgatgttt	cgcagctgcc	gtaagtgact	420
taccatgaac	ccctgacgta	tcttcttgtg	ggctcccagc	tgactggcca	atttaaggtg	480
cggcttgaac	ggagctctct	acttcgtgtc	catggacgcg	gatggtggcg	tgagcaagta	540
tcccaccaac	accgctggcg	ccaagtacgg	cacgggggtac	tgtgacagcc	agtgtcccgc	600
cgatctgaag	ttcatcaatg	gccaggccaa	cgttgagggc	tgaggagccgt	catccaacaa	660
cgcaaacacg	ggcattggag	gacacggaag	ctgctgctct	gagatggata	tctgggaggg	720
caactccatc	tccgaggctc	ttacccccca	cccttgacag	actgtcggcc	aggagatctg	780
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aagctttacc	ctcgatacca	ccaagaaatt	gaccgttgtc	acccagttcg	agacgtcggg	960
tgccatcaac	cgatactatg	tccagaatgg	cgtaactttc	cagcagccca	acgccgagct	1020
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ggactccacc	taccgacaa	acgagacctc	ctccacacc	ggtgccgtgc	gcggaagctg	1320
ctccaccagc	tccggtgtcc	ctgctcaggt	cgaatctcag	tctcccaacg	ccaaggtcac	1380
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<210> 4

<211> 81

<212> DNA

<213> *Trichoderma reesei*

<400> 4

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<210> 5

<211> 480

<212> PRT

<213> *Trichoderma reesei*

<400> 5

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Trp	Gln	Lys	Cys	Ser	Ser	Gly	Gly	Thr	Cys	Thr	Gln	Gln	Thr	Gly	Ser	35	40	45	
Val	Val	Ile	Asp	Ala	Asn	Trp	Arg	Trp	Thr	His	Ala	Thr	Asn	Ser	Ser	50	55	60	
Thr	Asn	Cys	Tyr	Asp	Gly	Asn	Thr	Trp	Ser	Ser	Thr	Leu	Cys	Pro	Asp	65	70	75	80
Asn	Glu	Thr	Cys	Ala	Lys	Asn	Cys	Cys	Leu	Asp	Gly	Ala	Ala	Tyr	Ala	85	90	95	
Ser	Thr	Tyr	Gly	Val	Thr	Thr	Ser	Gly	Asn	Ser	Leu	Ser	Ile	Gly	Phe	100	105	110	
Val	Thr	Gln	Ser	Ala	Gln	Lys	Asn	Val	Gly	Ala	Arg	Leu	Tyr	Leu	Met	115	120	125	
Ala	Ser	Asp	Thr	Thr	Tyr	Gln	Glu	Phe	Thr	Leu	Leu	Gly	Asn	Glu	Phe	130	135	140	
Ser	Phe	Asp	Val	Asp	Val	Ser	Gln	Leu	Pro	Cys	Gly	Leu	Asn	Gly	Ala	145	150	155	160
Leu	Tyr	Phe	Val	Ser	Met	Asp	Ala	Asp	Gly	Gly	Val	Ser	Lys	Tyr	Pro	165	170	175	
Thr	Asn	Thr	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	Ser	Gln	180	185	190	
Cys	Pro	Arg	Asp	Leu	Lys	Phe	Ile	Asn	Gly	Gln	Ala	Asn	Val	Glu	Gly	195	200	205	
Trp	Glu	Pro	Ser	Ser	Asn	Asn	Ala	Asn	Thr	Gly	Ile	Gly	Gly	His	Gly	210	215	220	
Ser	Cys	Cys	Ser	Glu	Met	Asp	Ile	Trp	Glu	Ala	Asn	Ser	Ile	Ser	Glu	225	230	235	240
Ala	Leu	Thr	Pro	His	Pro	Cys	Thr	Thr	Val	Gly	Gln	Glu	Ile	Cys	Glu	245	250	255	
Gly	Asp	Gly	Cys	Gly	Gly	Thr	Tyr	Ser	Asp	Asn	Arg	Tyr	Gly	Gly	Thr	260	265	270	
Cys	Asp	Pro	Asp	Gly	Cys	Asp	Trp	Asn	Pro	Tyr	Arg	Leu	Gly	Asn	Thr	275	280	285	
Ser	Phe	Tyr	Gly	Pro	Gly	Ser	Ser	Phe	Thr	Leu	Asp	Thr	Thr	Lys	Lys	290	295	300	
Leu	Thr	Val	Val	Thr	Gln	Phe	Glu	Thr	Ser	Gly	Ala	Ile	Asn	Arg	Tyr	305	310	315	320
Tyr	Val	Gln	Asn	Gly	Val	Thr	Phe	Gln	Gln	Pro	Asn	Ala	Glu	Leu	Gly	325	330	335	
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Phe	Lys	Lys	Ala	Thr	Ser	Gly	Gly	Met	Val	Leu	Val	Met	Ser	Leu	Trp	370	375	380	
Asp	Asp	Tyr	Tyr	Ala	Asn	Met	Leu	Trp	Leu	Asp	Ser	Thr	Tyr	Pro	Thr	385	390	395	400
Asn	Glu	Thr	Ser	Ser	Thr	Pro	Gly	Ala	Val	Arg	Gly	Ser	Cys	Ser	Thr	405	410	415	
Ser	Ser	Gly	Val	Pro	Ala	Gln	Val	Glu	Ser	Gln	Ser	Pro	Asn	Ala	Lys	420	425	430	
Val	Thr	Phe	Ser	Asn	Ile	Lys	Phe	Gly	Pro	Ile	Gly	Ser	Thr	Gly	Asn	435	440	445	
Pro	Ser	Gly	Gly	Asn	Pro	Pro	Gly	Gly	Asn	Pro	Pro	Gly	Thr	Thr	Thr				

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<211> 431
<212>  PRT
<213>  Trichoderma reesei

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Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
      20              25              30
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
      35              40              45
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
      50              55              60
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65              70              75              80
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
      85              90              95
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
      100             105             110
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
      115             120             125
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
      130             135             140
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145             150             155             160
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
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Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
      180             185             190
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
      195             200             205
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
      210             215             220
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225             230             235             240
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
      245             250             255
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
      260             265             270
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
      275             280             285
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
      290             295             300
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305             310             315             320
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
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Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
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Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
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Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn

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405					410					415									
Thr	Phe	Ser	Asn	Ile	Lys	Phe	Gly	Pro	Ile	Gly	Ser	Thr	Gly	Asn					
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145					150					155					160
Asn	Glu	Pro	His	Asp	Pro	Ala	Cys	Trp	Gly	Cys	Gly	Asp	Pro	Ser	Ile
				165					170						175
Asp	Trp	Arg	Leu	Ala	Ala	Glu	Arg	Ala	Gly	Asn	Ala	Val	Leu	Ser	Val
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Asn	Pro	Asn	Leu	Leu	Ile	Phe	Val	Glu	Gly	Val	Gln	Ser	Tyr	Asn	Gly
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Val	Val	Leu	Asn	Val	Pro	Asn	Arg	Leu	Val	Tyr	Ser	Ala	His	Asp	Tyr
225					230					235					240
Ala	Thr	Ser	Val	Tyr	Pro	Gln	Thr	Trp	Phe	Ser	Asp	Pro	Thr	Phe	Pro
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Gln	Asn	Ile	Ala	Pro	Val	Trp	Leu	Gly	Glu	Phe	Gly	Thr	Thr	Leu	Gln
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Ser	Thr	Thr	Asp	Gln	Thr	Trp	Leu	Lys	Thr	Leu	Val	Gln	Tyr	Leu	Arg
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Pro	Thr	Ala	Gln	Tyr	Gly	Ala	Asp	Ser	Phe	Gln	Trp	Thr	Phe	Trp	Ser
305					310					315					320
Trp	Asn	Pro	Asp	Ser	Gly	Asp	Thr	Gly	Gly	Ile	Leu	Lys	Asp	Asp	Trp
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Gln	Thr	Val	Asp	Thr	Val	Lys	Asp	Gly	Tyr	Leu	Ala	Pro	Ile	Lys	Ser
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		355													

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 <211> 1914  
 <212> DNA  
 <213> Acidothermus cellulolyticus

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acgtacggcg	cagtgaccgg	caactggacg ccgttcaaca acgcctggac gacgatggaa 240
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